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(54) Title: ATTACHMENT ENHANCED 293 CELLS

(57) Abstract

Attachment enhanced human embryonic kidney cells, 293, are provided. These cells have been modified to contain a selected mammalian scavenger gene, which has been found to improve the ability of these cells to attach in culture. The improved cells of the invention are useful in assays in which the unmodified 293 cells could be used.

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ATTACHMENT ENHANCED 293 CELLS

Field of the Invention

This invention relates generally to cell lines used in the recombinant production, screening or measurement of protein or protein interactions *in vitro*.

Background of the Invention

The primary human embryonic kidney (HEK) 293 cell line is a permanent line of cells transformed by sheared human adenovirus type 5 (Ad 5) DNA. The cells are particularly sensitive to human adenovirus, are highly permissive for adenovirus DNA, and contain and express the transforming genes of Ad5. This is a hypotriploid human cell line. See, F. Graham *et al.*, J. Gen. Virol., 36:59-72 (1977); T. Harrison *et al.*, Virology, 77:319-329 (1977).

This cell line, which is readily available from commercial sources, such as the American Type Culture Collection, is used extensively in *in vitro* assays, and for the production of recombinant proteins and viruses. However, in washing steps which are conventionally and repeatedly employed in such *in vitro* assays and other manipulations of these cells, the cells readily detach or are washed away from the plates or dishes in which the studies are performed. This problem typically results in inaccurate, unreliably low measurement or collection of the protein, peptide or interaction to which the assay is directed.

There remains a need in the art for a cell substrate useful in *in vitro* manipulations in genetic engineering, which permits the measurement of accurate results.

Brief Summary of the Invention

In one aspect, the invention provides improved HEK 293 cells, which cells are 293 cells which have been transfected with a mammalian macrophage scavenger receptor gene. Preferably, this gene is the human Type I or II macrophage scavenger receptor gene [SEQ ID NOS: 1 or 3].

In another aspect, the invention provides a method of enhancing the ability of HEK 293 cells to attach in tissue culture. This method involves the steps of

transfecting 293 cells with a selected mammalian macrophage scavenger receptor gene.

In yet another aspect, the invention provides a method of screening compounds for biological activity which involves screening the improved 293 cells of the invention. In this method, the improved 293 cells have been further transfected with a selected gene and are then screened for expression of the selected gene. The cells expressing the selected genes are incubated in the presence of a compound of unknown biological activity, and then screened for the ability of the compound to affect the expressed gene product or its function.

Other aspects and advantages of the present invention are described further in the following detailed description of the preferred embodiments thereof.

Brief Description of the Drawings

Fig. 1 provides the nucleic acid [SEQ ID NO:1] and amino acid [SEQ ID NO:2] sequences of the human macrophage scavenger receptor type I.

Fig. 2 provides the nucleic acid [SEQ ID NO:3] and amino acid [SEQ ID NO:4] sequences of the human macrophage scavenger receptor type II.

Detailed Description of the Invention

The present invention provides an improved human embryonic kidney cell line, 293. The inventors have surprisingly found that human embryonic kidney (HEK) 293 cells transfected with a mammalian macrophage scavenger receptor gene demonstrate an enhanced ability to attach to a solid support as compared to conventional, unmodified 293 cells. In contrast to unmodified 293 cells, the improved 293 cells of the invention are not as readily washed away as unmodified 293 cells under the normal conditions of biological assays. Thus, the improved 293 cells of the invention are particularly well suited for use in *in vitro* studies and other applications for which unmodified 293 cells may be used.

As used herein "solid support" is any surface used for culturing, for *in vitro* assays, and the like. For example, a typical solid support is a plastic tissue culture plate, or a multi-well plate, hollow fibers, a test tube, conventionally employed

plastic beads, glass beads, etc. Other solid supports are well known to those of skill in the art.

By "enhanced ability to attach" is meant that the transfected cells of this invention attach to the solid support with sufficient avidity to resist detachment which normally occurs with untransfected 293 cells caused by assay washing steps with buffer or growth medium. More specifically, the transfected cells of this invention because of the characteristic of enhanced attachment provide results of, for example, five times the cell number remaining after two washes as compared to the number of cells remaining following two washes of untransfected cells.

The human embryonic kidney cell line, 293, is readily available from the American Type Culture Collection, 12301 Parklawn Drive, Rockville, Maryland, U.S.A., under accession number ATCC CRL 1573. Also encompassed by this invention are progeny and derivatives of this cell line, which may be prepared using conventional techniques. See, Sambrook, Molecular Cloning: A Laboratory Manual, 2d ed., Cold Spring Harbor Press, Cold Spring Harbor, NY (1989).

According to this invention, these cells are modified by transfection with a selected mammalian macrophage scavenger receptor (MSR) gene. Currently, in a preferred embodiment, this gene is selected from a human MSR Type I or Type II gene, and most preferably, the gene is characterized by the sequence provided in GenBank, under accession number D90187 (MSR Type I) or D90188 (MSR Type II). The sequences [SEQ ID NO:1 and 2] of MSR Type I are provided in Fig. 1. The sequences [SEQ ID NO: 3 and 4] of MSR Type II are provided in Fig. 2. Both of these genes were obtained from the human monocytic cell line THR-1 following four days of phorbol ester treatment. These two gene sequences are differential splice variants of a single human gene, and are described in more detail in A. Matsumoto *et al.*, Proc. Natl. Acad. Sci. USA, 87:9133-9137 (1990), incorporated by reference herein.

It is anticipated that non-human homologs of MSR I or MSR II will be similarly useful in preparing the improved 293 cells according to the invention. Particularly desirable are the bovine [T. Kodama *et al.*, Proc. Natl. Acad. Sci. USA, 85:9238-9242 (1988)], murine [M. Freeman *et al.*, Proc. Natl. Acad. Sci. USA,

87:8810-8814 (1990)] and rabbit [P. E. Bickel and M. W. Freeman, J. Clin. Invest., 90:1450-1457 (1992)] homologs, each of which is at least 60-80% homologous with the human MSR genes. It is further anticipated that other human scavenger receptor genes, particularly other genes which are produced recombinantly or are differentially selective for oxidized or acetylation-modified low density lipoprotein (LDL) species or another desired lipoprotein species, will be similarly useful.

One of these genes, preferably a human MSR gene, is selected and cloned into an appropriate vector for use in transfecting the 293 cells. Generally, a suitable expression vector is one which contains control or regulatory sequences operably linked with the nucleic acid sequences of the gene. These regulatory sequences are capable of directing the expression of the gene product in the 293 cells. Suitable vectors and regulatory sequences are well known to those of skill in the art and this invention is not limited by the selection thereof.

For example, suitable vectors may be, or contain components from, viral vectors selected from simian virus SV40, retroviruses, bovine papilloma virus, vaccinia virus, and adenovirus, or commonly used bacterial vectors or commonly used mammalian expression vectors or integrative vectors which lead to a stable expression cell line. The vector used in the examples below is pCDN [N. Aiyar *et al.*, Mol. Cell. Biochem., 131:75-96 (1994)], which contains the promoter from cytomegalovirus, followed by a polycloning site and a polyadenylation site, the SV40 early enhancer, the human gene for dihydrofolate reductase, and a gene conferring resistance to neomycin.

Methods for introduction of a vector containing an MSR gene into mammalian cells are well known. Examples of suitable methods include, without limitation, dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei.

Sequences which contain selectable markers may also be transfected into the cell line. These markers may be contained on the vector containing the MSR gene, or may be separately transfected using conventional techniques, such as those

described herein. Selectable markers for mammalian cells are known in the art, and include for example, thymidine kinase, dihydrofolate reductase (together with methotrexate as a DHFR amplifier), aminoglycoside phosphotransferase, hydromycin B phosphotransferase, asparagine synthetase, adenosine deaminase, metallothionien, and antibiotic resistant genes such as neomycin. Other markers may be readily selected by one of skill in the art, as desired.

As described in more detail below, if the MSR transfected cell is desired for use in a screening assay, the cell may also be transfected with other genes. The additional gene(s) may, for example, encode a protein which will be screened for biological activity or for interaction with the MSR or another transfected gene.

Following transfection with the selected MSR gene (and optionally, any other gene), the cells are incubated in a suitable selection medium, e.g., Eagles MEM, Dulbecco's MEM or the like.

Once modified to contain the MSR gene, or another suitable gene, according to the methods described above, the improved 293 cells are particularly well suited for use in any assay in which an unmodified 293 cell may be used. However the use of the improved 293 cells of the invention will result in superior attachment, and thus, more accurate test results.

An exemplary use of the improved 293 cells of the invention includes the use of these cells in a method of screening compounds for biological activity. This method involves the use of the attachment enhanced 293 cells of the invention which have been further transfected with a selected gene sequence. These cells are subsequently screened for expression of the selected gene. The cells expressing these selected genes are then incubated in the presence of a compound of unknown biological activity and further assayed for the ability of the compound to affect the expressed gene product.

Similarly, the attachment enhanced 293 cells of the invention may be used to identify antagonists of the MSR gene, i.e., to develop agents for atherosclerosis. Suitable assays for identifying antagonists to an expressed gene product are well known to those of skill in the art. See, T. Kodama *et al.*, Nature, 343:531-535 (1990), A.M. Pearson *et al.*, J. Biol. Chem., 268:3554 (1993).

The surprising result of enhanced attachment demonstrated by 293 cells transfected with MSR genes is not demonstrated when other cells, such as Chinese Hamster Ovary (CHO) cells, are transfected with MSR I or MSR II. To the inventors' knowledge, no other cell line has demonstrated this result when transfected with MSR genes.

The following examples illustrate the preferred methods for preparing the modified 293 cells of the invention and uses therefor. These examples are illustrative only and are not intended to limit the scope of the invention.

Example 1 - Calcium phosphate transfection of macrophage scavenger receptor I and II into human embryonic kidney 293 cells

The macrophage scavenger receptor I or II cDNAs [SEQ ID NO:1 and 3, respectively] were subcloned into the mammalian expression vector pCDN in the correct orientation [N. Aiyar, Mol. Cell. Biochem., 131:75-86 (1994)].

The resulting construct containing the macrophage scavenger receptor I or II cDNA was used to transfect human embryonic kidney (HEK) 293 cells by calcium phosphate transfection. One day prior to the transfection, the HEK 293 cells were plated into 10 cm dishes at a density of 2 x 10^5 cells, so that the cells would be approximately 10% confluent within 24 hours. The cells were seeded into Eagle's Minimal Essential Medium (EMEM) supplemented with 2mM L-glutamine and 10% fetal bovine serum (FBS).

The DNA was prepared for transfection by sterile ethanol precipitation. Following ethanol precipitation, the DNA pellet was dried inside a tissue culture hood. The pellet was then resuspended in 450 µL of sterile water and 50 µL of 2.5 M $CaCl_2$. Ten µg of DNA were used per 10 cm dish. While gently swirling the DNA mixture, 500 µL of sterile 2x BBS (50mM N,N-bis 2-hydroxyethyl-2-aminoethane sulfonic acid, 280mM $NaCl_2$ and 1.5mM Na_2HPO_4) was added. The BBS/DNA-$CaCl_2$ solution was allowed to form a precipitate by sitting at room temperature for 10-20 minutes.

The solution was then gently mixed to ensure adequate suspension of the precipitate and then added dropwise into the 10 cm dish of cells. The plate was

gently swirled to distribute contents evenly. After a 12-16 hour incubation, the medium was carefully removed, and the cells were washed once with 5 ml of PBS (without Ca^{2+} or Mg^{2+}) followed by the addition of 10ml of EMEM supplemented with 2mM L-glutamine and 10% FBS.

Following an overnight incubation, the medium was removed, and the cells were carefully washed once with 5 ml of PBS (without Ca^{2+} or Mg^{2+}). To initiate selection, 10 ml of fresh EMEM with L-glutamine supplemented with 2 mM L-glutamine, 10% FBS and 0.4 mg/ml of geneticin (GIBCO-BRL) were added. Two or three days later, the medium was changed.

After approximately 2-3 weeks, each plate was examined under the microscope for small patches of growing cells. The patches were grown large enough to be seen as small spots on the bottom of the plate. Once at this stage, all of the medium was removed and

3 µL of trypsin was added directly to the patch of cells. By pipetting up and down several times, the patch of cells was transferred to a 24 well dish containing 1 ml of medium with geneticin. The cells were expanded from this 24 well stage to a 6 well plate or T-25 Flask. Because the 293 cells grow best in conditioned medium, cells were fed based on their rate of growth, but typically not more than once a week.

Example 2 - Comparison of transfected and untransfected 293 cells

To demonstrate the surprising results of the above transfection, and the greater accuracy obtained in using the transfected 293 cells in assays, transfected 293 cells of this invention and untransfected 293 cells were seeded at the same cell density (100,000 per well) into 24-well plastic tissue culture dishes. These cells were allowed to grow for two days before testing. Cell growth appeared to be equivalent.

The same biochemical assay was performed on the transfected and untransfected cells.

The presence of macrophage scavenger receptors was confirmed by incubating transfected 293 cells with ^{125}[I]-acetylated LDL at a concentration of approximately 5 µg/ml (specific activity ~100-300 cpm/ng protein) for 5 hours at

37°C, essentially as described in J. Ashkenas *et al.*, J. Lipid Res., 34:983-1000 (1993). In replicate experiments, ^{125}[I]-acetylated LDL binding/uptake amounted to an average of 1.75µg/mg protein (n=76). Where it has been possible to measure ^{125}[I]-acetylated LDL binding/uptake to untransfected 293 cells, the average was 0.20 µg/mg protein (n=6). After the assays were performed on the cells, they were dissolved in 0.1 M NaOH, and aliquots were used to determine total protein concentration by the Pierce BCA assay with bovine serum albumin as the standard. In an attempt to keep as many untranfected cells as possible attached to the culture dished, the untransfected cells were washed only twice, while the transfected cells were washed seven times as per the procedure cited above.

Superior attachment of the transfected cells was observed in a comparison of recoverable protein, with an average of 113±2.3 µg protein/well (n=24) versus the untransfected cells with an average of 21.8±4.8 µg protein/well (n=12).

Numerous modifications and variations of the present invention are included in the above-identified specification and are expected to be obvious to one of skill in the art. Such modifications and alterations to the compositions and processes of the present invention are believed to be encompassed in the scope of the claims appended hereto.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

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Brawner, Mary E.

(ii) TITLE OF INVENTION: Attachment Enhanced 293 Cells

(iii) NUMBER OF SEQUENCES: 4

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(F) ZIP: 19406-5090

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(vi) CURRENT APPLICATION DATA:
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(B) FILING DATE:
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:
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(B) REGISTRATION NUMBER: 31,171
(C) REFERENCE/DOCKET NUMBER: SBC-P50338

(ix) TELECOMMUNICATION INFORMATION:
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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2028 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: cDNA to mRNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 47..1402

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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TCT GTG AAA TTT GAT GCT CGC TCA ATG ACA GCT TTG CTT CCT CCG AAT          151
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 20                  25                  30                  35

CCT AAA AAC AGC CCT TCC CTT CAA GAG AAA CTG AAG TCC TTC AAA GCT          199
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GCA CTG ATT GCC CTT TAC CTC CTC GTG TTT GCA GTT CTC ATC CCT CTC          247
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         70                  75                  80

TCA GTT AGT TCA ACT AAT GCA AAT GAT ATA ACT CAA AGT CTC ACG GGA          343
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     85                  90                  95
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GAA GCC AAC CTC ATG GAC ACA GAG CAT TTC CAA AAT TTC AGC ATG ACA      487
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    325                 330                 335

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                360                 365                 370

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Phe Gly Arg Glu Ser Ser Ile Glu Glu Cys Lys Ile Arg Gln Trp Gly
420                 425                 430                 435
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ACA AGA GCC TGT TCA CAT TCT GAA GAT GCT GGA GTC ACT TGC ACT TTA      1399
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GGAAGGGATC AGAAGATATC TTTTGTGCCT AGATTGCAAA ATCTCCAATC CACACATATT   1872

GTTTTAAAAT AAGAATGTTA TCCAACTATT AAGATATCTC AATGTGCAAT AACTTGTGTA   1932

TTAGATATCA ATGTTAATGA TATGTCTTGG CCACTATGGA CCAGGGAGCT TATTTTTCTT   1992

GTCATGTACT GACAACTGTT TAATTGAATC ATGAAG                             2028
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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 452 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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Met Glu Gln Trp Asp His Phe His Asn Gln Gln Glu Asp Thr Asp Ser
 1               5                  10                  15
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Cys Ser Glu Ser Val Lys Phe Asp Ala Arg Ser Met Thr Ala Leu Leu
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Pro Pro Asn Pro Lys Asn Ser Pro Ser Leu Gln Glu Lys Leu Lys Ser
        35                  40                  45

Phe Lys Ala Ala Leu Ile Ala Leu Tyr Leu Leu Val Phe Ala Val Leu
    50                  55                  60

Ile Pro Leu Ile Gly Ile Val Ala Ala Gln Leu Leu Lys Trp Glu Thr
65                  70                  75                  80

Lys Asn Cys Ser Val Ser Ser Thr Asn Ala Asn Asp Ile Thr Gln Ser
                85                  90                  95

Leu Thr Gly Lys Gly Asn Asp Ser Glu Glu Glu Met Arg Phe Gln Glu
            100                 105                 110

Val Phe Met Glu His Met Ser Asn Met Glu Lys Arg Ile Gln His Ile
        115                 120                 125

Leu Asp Met Glu Ala Asn Leu Met Asp Thr Glu His Phe Gln Asn Phe
    130                 135                 140

Ser Met Thr Thr Asp Gln Arg Phe Asn Asp Ile Leu Leu Gln Leu Ser
145                 150                 155                 160

Thr Leu Phe Ser Ser Val Gln Gly His Gly Asn Ala Ile Asp Glu Ile
                165                 170                 175

Ser Lys Ser Leu Ile Ser Leu Asn Thr Thr Leu Leu Asp Leu Gln Leu
            180                 185                 190

Asn Ile Glu Asn Leu Asn Gly Lys Ile Gln Glu Asn Thr Phe Lys Gln
        195                 200                 205

Gln Glu Glu Ile Ser Lys Leu Glu Glu Arg Val Tyr Asn Val Ser Ala
    210                 215                 220

Glu Ile Met Ala Met Lys Glu Glu Gln Val His Leu Glu Gln Glu Ile
225                 230                 235                 240
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Lys Gly Glu Val Lys Val Leu Asn Asn Ile Thr Asn Asp Leu Arg Leu
                245                 250                 255

Lys Asp Trp Glu His Ser Gln Thr Leu Arg Asn Ile Thr Leu Ile Gln
            260                 265                 270

Gly Pro Pro Gly Pro Pro Gly Glu Lys Gly Asp Arg Gly Pro Thr Gly
        275                 280                 285

Glu Ser Gly Pro Arg Gly Phe Pro Gly Pro Ile Gly Pro Pro Gly Leu
    290                 295                 300

Lys Gly Asp Arg Gly Ala Ile Gly Phe Pro Gly Ser Arg Gly Leu Pro
305                 310                 315                 320

Gly Tyr Ala Gly Arg Pro Gly Asn Ser Gly Pro Lys Gly Gln Lys Gly
                325                 330                 335

Glu Lys Gly Ser Gly Asn Thr Leu Thr Pro Phe Thr Lys Val Arg Leu
            340                 345                 350

Val Gly Gly Ser Gly Pro His Glu Gly Arg Val Glu Ile Leu His Ser
        355                 360                 365

Gly Gln Trp Gly Thr Ile Cys Asp Asp Arg Trp Glu Val Arg Val Gly
    370                 375                 380

Gln Val Val Cys Arg Ser Leu Gly Tyr Pro Gly Val Gln Ala Val His
385                 390                 395                 400

Lys Ala Ala His Phe Gly Gln Gly Thr Gly Pro Ile Trp Leu Asn Glu
                405                 410                 415

Val Phe Cys Phe Gly Arg Glu Ser Ser Ile Glu Glu Cys Lys Ile Arg
            420                 425                 430

Gln Trp Gly Thr Arg Ala Cys Ser His Ser Glu Asp Ala Gly Val Thr
        435                 440                 445

Cys Thr Leu  *
    450
```

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1367 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: cDNA to mRNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 67..1143

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```
TAGGTTTCAA TTGTAAAGAG AGAGAAGTGG ATAAATCAGT GCTGCTTTCT TTAGGACGAA      60

AGAAGT ATG GAG CAG TGG GAT CAC TTT CAC AAT CAA CAG GAG GAC ACT          108
       Met Glu Gln Trp Asp His Phe His Asn Gln Gln Glu Asp Thr
         1               5                  10

GAT AGC TGC TCC GAA TCT GTG AAA TTT GAT GCT CGC TCA ATG ACA GCT         156
Asp Ser Cys Ser Glu Ser Val Lys Phe Asp Ala Arg Ser Met Thr Ala
 15                  20                  25                  30

TTG CTT CCT CCG AAT CCT AAA AAC AGC CCT TCC CTT CAA GAG AAA CTG         204
Leu Leu Pro Pro Asn Pro Lys Asn Ser Pro Ser Leu Gln Glu Lys Leu
                 35                  40                  45

AAG TCC TTC AAA GCT GCA CTG ATT GCC CTT TAC CTC CTC GTG TTT GCA         252
Lys Ser Phe Lys Ala Ala Leu Ile Ala Leu Tyr Leu Leu Val Phe Ala
             50                  55                  60

GTT CTC ATC CCT CTC ATT GGA ATA GTG GCA GCT CAA CTC CTG AAG TGG         300
Val Leu Ile Pro Leu Ile Gly Ile Val Ala Ala Gln Leu Leu Lys Trp
         65                  70                  75

GAA ACG AAG AAT TGC TCA GTT AGT TCA ACT AAT GCA AAT GAT ATA ACT         348
Glu Thr Lys Asn Cys Ser Val Ser Ser Thr Asn Ala Asn Asp Ile Thr
     80                  85                  90
```

```
CAA AGT CTC ACG GGA AAA GGA AAT GAC AGC GAA GAG GAA ATG AGA TTT      396
Gln Ser Leu Thr Gly Lys Gly Asn Asp Ser Glu Glu Glu Met Arg Phe
 95                 100                 105                 110

CAA GAA GTC TTT ATG GAA CAC ATG AGC AAC ATG GAG AAG AGA ATC CAG      444
Gln Glu Val Phe Met Glu His Met Ser Asn Met Glu Lys Arg Ile Gln
                115                 120                 125

CAT ATT TTA GAC ATG GAA GCC AAC CTC ATG GAC ACA GAG CAT TTC CAA      492
His Ile Leu Asp Met Glu Ala Asn Leu Met Asp Thr Glu His Phe Gln
            130                 135                 140

AAT TTC AGC ATG ACA ACT GAT CAA AGA TTT AAT GAC ATT CTT CTG CAG      540
Asn Phe Ser Met Thr Thr Asp Gln Arg Phe Asn Asp Ile Leu Leu Gln
        145                 150                 155

CTA AGT ACC TTG TTT TCC TCA GTC CAG GGA CAT GGG AAT GCA ATA GAT      588
Leu Ser Thr Leu Phe Ser Ser Val Gln Gly His Gly Asn Ala Ile Asp
    160                 165                 170

GAA ATC TCC AAG TCC TTA ATA AGT TTG AAT ACC ACA TTG CTT GAT TTG      636
Glu Ile Ser Lys Ser Leu Ile Ser Leu Asn Thr Thr Leu Leu Asp Leu
175                 180                 185                 190

CAG CTC AAC ATA GAA AAT CTG AAT GGC AAA ATC CAA GAG AAT ACC TTC      684
Gln Leu Asn Ile Glu Asn Leu Asn Gly Lys Ile Gln Glu Asn Thr Phe
                195                 200                 205

AAA CAA CAA GAG GAA ATC AGT AAA TTA GAG GAG CGT GTT TAC AAT GTA      732
Lys Gln Gln Glu Glu Ile Ser Lys Leu Glu Glu Arg Val Tyr Asn Val
            210                 215                 220

TCA GCA GAA ATT ATG GCT ATG AAA GAA GAA CAA GTG CAT TTG GAA CAG      780
Ser Ala Glu Ile Met Ala Met Lys Glu Glu Gln Val His Leu Glu Gln
        225                 230                 235

GAA ATA AAA GGA GAA GTG AAA GTA CTG AAT AAC ATC ACT AAT GAT CTC      828
Glu Ile Lys Gly Glu Val Lys Val Leu Asn Asn Ile Thr Asn Asp Leu
    240                 245                 250

AGA CTG AAA GAT TGG GAA CAT TCT CAG ACC TTG AGA AAT ATC ACT TTA      876
Arg Leu Lys Asp Trp Glu His Ser Gln Thr Leu Arg Asn Ile Thr Leu
255                 260                 265                 270
```

```
ATT CAA GGT CCT CCT GGA CCC CCG GGT GAA AAA GGA GAT CGA GGT CCC      924
Ile Gln Gly Pro Pro Gly Pro Pro Gly Glu Lys Gly Asp Arg Gly Pro
                275                 280                 285

ACT GGA GAA AGT GGT CCA CGA GGA TTT CCA GGT CCA ATA GGT CCT CCG      972
Thr Gly Glu Ser Gly Pro Arg Gly Phe Pro Gly Pro Ile Gly Pro Pro
            290                 295                 300

GGT CTT AAA GGT GAT CGG GGA GCA ATT GGC TTT CCT GGA AGT CGA GGA     1020
Gly Leu Lys Gly Asp Arg Gly Ala Ile Gly Phe Pro Gly Ser Arg Gly
        305                 310                 315

CTC CCA GGA TAT GCC GGA AGG CCA GGA AAT TCT GGA CCA AAA GGC CAG     1068
Leu Pro Gly Tyr Ala Gly Arg Pro Gly Asn Ser Gly Pro Lys Gly Gln
    320                 325                 330

AAA GGG GAA AAG GGG AGT GGA AAC ACA TTA AGA CCA GTA CAA CTC ACT     1116
Lys Gly Glu Lys Gly Ser Gly Asn Thr Leu Arg Pro Val Gln Leu Thr
335                 340                 345                 350

GAT CAT ATT AGG GCA GGG CCC TCT TAA GATCAGGTGG GTTGGGCGGG           1163
Asp His Ile Arg Ala Gly Pro Ser  *
                355

ACATCCTCTG CTACCATCTC ATTAAAAGGC CCTTCACCTC TGGACAAGTC ATCTGCAACA   1223

ACTGACTTCC AAGATCCTTT TGTGACTCCT CCAAATGACT TTGGTTCCCG TGTTGTACCT   1283

GACTTCCACA TGGCCTTCTC TCCTGGTCCC TGGTGCTGTT TGGGCCTCTG CTCCCATGCT   1343

CATACCTCTT CTTACTCCAA TTAC                                          1367
```

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 359 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```
Met Glu Gln Trp Asp His Phe His Asn Gln Gln Glu Asp Thr Asp Ser
 1               5                  10                  15

Cys Ser Glu Ser Val Lys Phe Asp Ala Arg Ser Met Thr Ala Leu Leu
            20                  25                  30

Pro Pro Asn Pro Lys Asn Ser Pro Ser Leu Gln Glu Lys Leu Lys Ser
        35                  40                  45

Phe Lys Ala Ala Leu Ile Ala Leu Tyr Leu Leu Val Phe Ala Val Leu
    50                  55                  60

Ile Pro Leu Ile Gly Ile Val Ala Ala Gln Leu Leu Lys Trp Glu Thr
65                  70                  75                  80

Lys Asn Cys Ser Val Ser Ser Thr Asn Ala Asn Asp Ile Thr Gln Ser
                85                  90                  95

Leu Thr Gly Lys Gly Asn Asp Ser Glu Glu Glu Met Arg Phe Gln Glu
            100                 105                 110

Val Phe Met Glu His Met Ser Asn Met Glu Lys Arg Ile Gln His Ile
        115                 120                 125

Leu Asp Met Glu Ala Asn Leu Met Asp Thr Glu His Phe Gln Asn Phe
    130                 135                 140

Ser Met Thr Thr Asp Gln Arg Phe Asn Asp Ile Leu Leu Gln Leu Ser
145                 150                 155                 160

Thr Leu Phe Ser Ser Val Gln Gly His Gly Asn Ala Ile Asp Glu Ile
                165                 170                 175

Ser Lys Ser Leu Ile Ser Leu Asn Thr Thr Leu Leu Asp Leu Gln Leu
            180                 185                 190

Asn Ile Glu Asn Leu Asn Gly Lys Ile Gln Glu Asn Thr Phe Lys Gln
        195                 200                 205

Gln Glu Glu Ile Ser Lys Leu Glu Glu Arg Val Tyr Asn Val Ser Ala
    210                 215                 220
```

```
Glu Ile Met Ala Met Lys Glu Glu Gln Val His Leu Glu Gln Glu Ile
225                 230                 235                 240

Lys Gly Glu Val Lys Val Leu Asn Asn Ile Thr Asn Asp Leu Arg Leu
                245                 250                 255

Lys Asp Trp Glu His Ser Gln Thr Leu Arg Asn Ile Thr Leu Ile Gln
            260                 265                 270

Gly Pro Pro Gly Pro Pro Gly Glu Lys Gly Asp Arg Gly Pro Thr Gly
        275                 280                 285

Glu Ser Gly Pro Arg Gly Phe Pro Gly Pro Ile Gly Pro Pro Gly Leu
    290                 295                 300

Lys Gly Asp Arg Gly Ala Ile Gly Phe Pro Gly Ser Arg Gly Leu Pro
305                 310                 315                 320

Gly Tyr Ala Gly Arg Pro Gly Asn Ser Gly Pro Lys Gly Gln Lys Gly
                325                 330                 335

Glu Lys Gly Ser Gly Asn Thr Leu Arg Pro Val Gln Leu Thr Asp His
            340                 345                 350

Ile Arg Ala Gly Pro Ser  *
        355
```

WHAT IS CLAIMED IS:

1. Human embryonic kidney 293 cells transfected with a mammalian scavenger receptor gene, said cells demonstrating an enhanced ability to attach to a solid support.

2. The cells according to claim 1 wherein said receptor gene is a human macrophage scavenger receptor gene Type I.

3. The cells according to claim 1 wherein the receptor gene is characterized by the sequence of GenBank accession number D90187.

4. The cells according to claim 1 wherein said receptor gene is a human macrophage scavenger receptor gene Type II.

5. The cells according to claim 1 wherein the receptor gene is characterized by the sequence of GenBank accession number D90188.

6. The cells according to claim 1 wherein said receptor gene is a macrophage scavenger receptor gene of a non-human species.

7. A solid support to which is attached human embryonic kidney 293 cells transfected with a mammalian scavenger receptor gene.

8. The support according to claim 7 wherein said receptor gene is a human macrophage scavenger receptor gene Type I.

9. The support according to claim 7 wherein the receptor gene is characterized by the sequence of GenBank accession number D90187.

10. The support according to claim 7 wherein said receptor gene is a human macrophage scavenger receptor gene Type II.

11. The support according to claim 7 wherein the receptor gene is characterized by the sequence of GenBank accession number D90188.

12. The support according to claim 7 wherein said receptor gene is a macrophage scavenger receptor gene of a non-human species.

13. A method of enhancing the ability of human embryonic kidney cells to attach to a solid support comprising the steps of:

(a) providing cells from a 293 cell line; and

(b) transfecting the cells with a mammalian scavenger receptor gene;

wherein the transfected cells are characterized by an enhanced ability to attach to said solid support.

14. The method according to claim 13 further comprising transfecting said cells with a second selected gene.

15. The method according to claim 14 wherein the selected gene is a selection marker.

16. The method according to claim 15 wherein the gene is a selectable resistance marker.

17. A method of screening a compounds for biological activity comprising the steps of:

(a) providing on a solid support human embryonic kidney 293 cells co-transfected with a mammalian scavenger receptor gene and a second selected gene which encodes a protein having a biological activity;

(b) measuring expression of the protein encoded by said second selected gene;

(c) incubating said co-transfected 293 cells in the presence of a compound of unknown biological activity;

(d) screening the cells of (c) for the ability of the compound to alter said biological activity.

18. The method according to claim 17 wherein the receptor gene is a human macrophage scavenger receptor gene Type I or Type II.

19. An improved method for screening a compound for biological activity comprising measuring in a transfected cell the expression of a protein encoded by a selected gene; incubating said transfected cell in the presence of a compound of unknown biological activity; and screening the cell for the ability of said compound to alter said biological activity, the improvement comprising employing as said transfected cell, human embryonic kidney 293 cells co-transfected with a mammalian scavenger receptor gene and said selected gene, said cells attached to a solid support.

20. An improved method for performing a biological assay on a cell attached to a solid support, wherein said assay involves at least one washing step, said improvement comprising employing as said attached cell, human embryonic kidney 293 cells co-transfected with a mammalian scavenger receptor gene.

21. An improved method for measuring the production of a protein in a cell attached to a solid support, said improvement comprising employing as said attached cell, human embryonic kidney 293 cells co-transfected with a mammalian scavenger receptor gene.

Human Macrophage Scavenger Receptor Type I
Nucleic acid SEQ ID NO:1 and Amino Acid SEQ ID NO:2 Sequences

```
AGAGAAGTGG ATAAATCAGT GCTGCTTTCT TTAGGACGAA AGAAGT ATG GAG CAG          55
                                                    Met Glu Gln
                                                     1

TGG GAT CAC TTT CAC AAT CAA CAG GAG GAC ACT GAT AGC TGC TCC GAA         103
Trp Asp His Phe His Asn Gln Gln Glu Asp Thr Asp Ser Cys Ser Glu
  5                  10                  15

TCT GTG AAA TTT GAT GCT CGC TCA ATG ACA GCT TTG CTT CCT CCG AAT         151
Ser Val Lys Phe Asp Ala Arg Ser Met Thr Ala Leu Leu Pro Pro Asn
 20                  25                  30                  35

CCT AAA AAC AGC CCT TCC CTT CAA GAG AAA CTG AAG TCC TTC AAA GCT         199
Pro Lys Asn Ser Pro Ser Leu Gln Glu Lys Leu Lys Ser Phe Lys Ala
                 40                  45                  50

GCA CTG ATT GCC CTT TAC CTC CTC GTG TTT GCA GTT CTC ATC CCT CTC         247
Ala Leu Ile Ala Leu Tyr Leu Leu Val Phe Ala Val Leu Ile Pro Leu
           55                  60                  65

ATT GGA ATA GTG GCA GCT CAA CTC CTG AAG TGG GAA ACG AAG AAT TGC         295
Ile Gly Ile Val Ala Ala Gln Leu Leu Lys Trp Glu Thr Lys Asn Cys
     70                  75                  80

TCA GTT AGT TCA ACT AAT GCA AAT GAT ATA ACT CAA AGT CTC ACG GGA         343
Ser Val Ser Ser Thr Asn Ala Asn Asp Ile Thr Gln Ser Leu Thr Gly
  85                  90                  95

AAA GGA AAT GAC AGC GAA GAG GAA ATG AGA TTT CAA GAA GTC TTT ATG         391
Lys Gly Asn Asp Ser Glu Glu Glu Met Arg Phe Gln Glu Val Phe Met
100                 105                 110                 115

GAA CAC ATG AGC AAC ATG GAG AAG AGA ATC CAG CAT ATT TTA GAC ATG         439
Glu His Met Ser Asn Met Glu Lys Arg Ile Gln His Ile Leu Asp Met
                120                 125                 130

GAA GCC AAC CTC ATG GAC ACA GAG CAT TTC CAA AAT TTC AGC ATG ACA         487
Glu Ala Asn Leu Met Asp Thr Glu His Phe Gln Asn Phe Ser Met Thr
           135                 140                 145

ACT GAT CAA AGA TTT AAT GAC ATT CTT CTG CAG CTA AGT ACC TTG TTT         535
Thr Asp Gln Arg Phe Asn Asp Ile Leu Leu Gln Leu Ser Thr Leu Phe
     150                 155                 160

TCC TCA GTC CAG GGA CAT GGG AAT GCA ATA GAT GAA ATC TCC AAG TCC         583
Ser Ser Val Gln Gly His Gly Asn Ala Ile Asp Glu Ile Ser Lys Ser
165                 170                 175

TTA ATA AGT TTG AAT ACC ACA TTG CTT GAT TTG CAG CTC AAC ATA GAA         631
Leu Ile Ser Leu Asn Thr Thr Leu Leu Asp Leu Gln Leu Asn Ile Glu
180                 185                 190                 195

AAT CTG AAT GGC AAA ATC CAA GAG AAT ACC TTC AAA CAA CAA GAG GAA         679
Asn Leu Asn Gly Lys Ile Gln Glu Asn Thr Phe Lys Gln Gln Glu Glu
                200                 205                 210
```

Fig. 1A

```
ATC AGT AAA TTA GAG GAG CGT GTT TAC AAT GTA TCA GCA GAA ATT ATG      727
Ile Ser Lys Leu Glu Glu Arg Val Tyr Asn Val Ser Ala Glu Ile Met
            215                 220                 225

GCT ATG AAA GAA GAA CAA GTG CAT TTG GAA CAG GAA ATA AAA GGA GAA      775
Ala Met Lys Glu Glu Gln Val His Leu Glu Gln Glu Ile Lys Gly Glu
        230                 235                 240

GTG AAA GTA CTG AAT AAC ATC ACT AAT GAT CTC AGA CTG AAA GAT TGG      823
Val Lys Val Leu Asn Asn Ile Thr Asn Asp Leu Arg Leu Lys Asp Trp
    245                 250                 255

GAA CAT TCT CAG ACC TTG AGA AAT ATC ACT TTA ATT CAA GGT CCT CCT      871
Glu His Ser Gln Thr Leu Arg Asn Ile Thr Leu Ile Gln Gly Pro Pro
260                 265                 270                 275

GGA CCC CCG GGT GAA AAA GGA GAT CGA GGT CCC ACT GGA GAA AGT GGT      919
Gly Pro Pro Gly Glu Lys Gly Asp Arg Gly Pro Thr Gly Glu Ser Gly
                280                 285                 290

CCA CGA GGA TTT CCA GGT CCA ATA GGT CCT CCG GGT CTT AAA GGT GAT      967
Pro Arg Gly Phe Pro Gly Pro Ile Gly Pro Pro Gly Leu Lys Gly Asp
            295                 300                 305

CGG GGA GCA ATT GGC TTT CCT GGA AGT CGA GGA CTC CCA GGA TAT GCC     1015
Arg Gly Ala Ile Gly Phe Pro Gly Ser Arg Gly Leu Pro Gly Tyr Ala
        310                 315                 320

GGA AGG CCA GGA AAT TCT GGA CCA AAA GGC CAG AAA GGG GAA AAG GGG     1063
Gly Arg Pro Gly Asn Ser Gly Pro Lys Gly Gln Lys Gly Glu Lys Gly
    325                 330                 335

AGT GGA AAC ACA TTA ACT CCA TTT ACG AAA GTT CGA CTG GTC GGT GGG     1111
Ser Gly Asn Thr Leu Thr Pro Phe Thr Lys Val Arg Leu Val Gly Gly
340                 345                 350                 355

AGC GGC CCT CAC GAG GGG AGA GTG GAG ATA CTC CAC AGC GGC CAG TGG     1159
Ser Gly Pro His Glu Gly Arg Val Glu Ile Leu His Ser Gly Gln Trp
                360                 365                 370

GGT ACA ATT TGT GAC GAT CGC TGG GAA GTG CGC GTT GGA CAG GTC GTC     1207
Gly Thr Ile Cys Asp Asp Arg Trp Glu Val Arg Val Gly Gln Val Val
            375                 380                 385

TGT AGG AGC TTG GGA TAC CCA GGT GTT CAA GCC GTG CAC AAG GCA GCT     1255
Cys Arg Ser Leu Gly Tyr Pro Gly Val Gln Ala Val His Lys Ala Ala
        390                 395                 400

CAC TTT GGA CAA GGT ACT GGT CCA ATA TGG CTG AAT GAA GTG TTT TGT     1303
His Phe Gly Gln Gly Thr Gly Pro Ile Trp Leu Asn Glu Val Phe Cys
    405                 410                 415

TTT GGG AGA GAA TCA TCT ATT GAA GAA TGT AAA ATT CGG CAA TGG GGG     1351
Phe Gly Arg Glu Ser Ser Ile Glu Glu Cys Lys Ile Arg Gln Trp Gly
420                 425                 430                 435

ACA AGA GCC TGT TCA CAT TCT GAA GAT GCT GGA GTC ACT TGC ACT TTA     1399
Thr Arg Ala Cys Ser His Ser Glu Asp Ala Gly Val Thr Cys Thr Leu
                440                 445                 450
```

Fig. 1B

```
TAA TGCATCATAT TTTCATTCAC AACTATGAAA TCGCTGCTCA AAAATGATTT          1452
 *

TATTACCTTG TTCCTGTAAA ATCCATTTAA TCAATATTTA AGAGATTAAG AATATTGCCC  1512

AAATAATATT TTAGATTACA GGATTAATAT ATTGAACACC TTCATGCTTA CTATTTTATG  1572

TCTATATTTA AATCATTTTA ACTTCTATAG GTTTTTAAAT GGAATTTTCT AATATAATGA  1632

CTTATATGCT GAATTGAACA TTTTGAAGTT TATAGCTTCC AGATTACAAA GGCCAAGGGT  1692

AATAGAAATG CATACCAGTA ATTGGCTCCA ATTCATAATA TGTTCACCAG GAGATTACAA  1752

TTTTTTGCTC TTCTTGTCTT TGTAATCTAT TTAGTTGATT TTAATTACTT TCTGAATAAC  1812

GGAAGGGATC AGAAGATATC TTTTGTGCCT AGATTGCAAA ATCTCCAATC CACACATATT  1872

GTTTTAAAAT AAGAATGTTA TCCAACTATT AAGATATCTC AATGTGCAAT AACTTGTGTA  1932

TTAGATATCA ATGTTAATGA TATGTCTTGG CCACTATGGA CCAGGGAGCT TATTTTTCTT  1992

GTCATGTACT GACAACTGTT TAATTGAATC ATGAAG                            2028
```

Fig. 1C

Human Macrophage Scavenger Receptor Type II
Nucleic acid SEQ ID NO:3 and Amino Acid SEQ ID NO:4 Sequences

```
TAGGTTTCAA TTGTAAAGAG AGAGAAGTGG ATAAATCAGT GCTGCTTTCT TTAGGACGAA      60

AGAAGT ATG GAG CAG TGG GAT CAC TTT CAC AAT CAA CAG GAG GAC ACT         108
       Met Glu Gln Trp Asp His Phe His Asn Gln Gln Glu Asp Thr
         1               5                  10

GAT AGC TGC TCC GAA TCT GTG AAA TTT GAT GCT CGC TCA ATG ACA GCT        156
Asp Ser Cys Ser Glu Ser Val Lys Phe Asp Ala Arg Ser Met Thr Ala
 15                  20                  25                  30

TTG CTT CCT CCG AAT CCT AAA AAC AGC CCT TCC CTT CAA GAG AAA CTG        204
Leu Leu Pro Pro Asn Pro Lys Asn Ser Pro Ser Leu Gln Glu Lys Leu
                 35                  40                  45

AAG TCC TTC AAA GCT GCA CTG ATT GCC CTT TAC CTC CTC GTG TTT GCA        252
Lys Ser Phe Lys Ala Ala Leu Ile Ala Leu Tyr Leu Leu Val Phe Ala
             50                  55                  60

GTT CTC ATC CCT CTC ATT GGA ATA GTG GCA GCT CAA CTC CTG AAG TGG        300
Val Leu Ile Pro Leu Ile Gly Ile Val Ala Ala Gln Leu Leu Lys Trp
         65                  70                  75

GAA ACG AAG AAT TGC TCA GTT AGT TCA ACT AAT GCA AAT GAT ATA ACT        348
Glu Thr Lys Asn Cys Ser Val Ser Ser Thr Asn Ala Asn Asp Ile Thr
     80                  85                  90

CAA AGT CTC ACG GGA AAA GGA AAT GAC AGC GAA GAG GAA ATG AGA TTT        396
Gln Ser Leu Thr Gly Lys Gly Asn Asp Ser Glu Glu Glu Met Arg Phe
 95                  100                 105                 110

CAA GAA GTC TTT ATG GAA CAC ATG AGC AAC ATG GAG AAG AGA ATC CAG        444
Gln Glu Val Phe Met Glu His Met Ser Asn Met Glu Lys Arg Ile Gln
                115                 120                 125

CAT ATT TTA GAC ATG GAA GCC AAC CTC ATG GAC ACA GAG CAT TTC CAA        492
His Ile Leu Asp Met Glu Ala Asn Leu Met Asp Thr Glu His Phe Gln
            130                 135                 140

AAT TTC AGC ATG ACA ACT GAT CAA AGA TTT AAT GAC ATT CTT CTG CAG        540
Asn Phe Ser Met Thr Thr Asp Gln Arg Phe Asn Asp Ile Leu Leu Gln
        145                 150                 155

CTA AGT ACC TTG TTT TCC TCA GTC CAG GGA CAT GGG AAT GCA ATA GAT        588
Leu Ser Thr Leu Phe Ser Ser Val Gln Gly His Gly Asn Ala Ile Asp
    160                 165                 170

GAA ATC TCC AAG TCC TTA ATA AGT TTG AAT ACC ACA TTG CTT GAT TTG        636
Glu Ile Ser Lys Ser Leu Ile Ser Leu Asn Thr Thr Leu Leu Asp Leu
175                 180                 185                 190

CAG CTC AAC ATA GAA AAT CTG AAT GGC AAA ATC CAA GAG AAT ACC TTC        684
Gln Leu Asn Ile Glu Asn Leu Asn Gly Lys Ile Gln Glu Asn Thr Phe
                195                 200                 205
```

Fig. 2A

```
AAA CAA CAA GAG GAA ATC AGT AAA TTA GAG GAG CGT GTT TAC AAT GTA        732
Lys Gln Gln Glu Glu Ile Ser Lys Leu Glu Glu Arg Val Tyr Asn Val
            210                 215                 220

TCA GCA GAA ATT ATG GCT ATG AAA GAA GAA CAA GTG CAT TTG GAA CAG        780
Ser Ala Glu Ile Met Ala Met Lys Glu Glu Gln Val His Leu Glu Gln
        225                 230                 235

GAA ATA AAA GGA GAA GTG AAA GTA CTG AAT AAC ATC ACT AAT GAT CTC        828
Glu Ile Lys Gly Glu Val Lys Val Leu Asn Asn Ile Thr Asn Asp Leu
    240                 245                 250

AGA CTG AAA GAT TGG GAA CAT TCT CAG ACC TTG AGA AAT ATC ACT TTA        876
Arg Leu Lys Asp Trp Glu His Ser Gln Thr Leu Arg Asn Ile Thr Leu
255                 260                 265                 270

ATT CAA GGT CCT CCT GGA CCC CCG GGT GAA AAA GGA GAT CGA GGT CCC        924
Ile Gln Gly Pro Pro Gly Pro Pro Gly Glu Lys Gly Asp Arg Gly Pro
                275                 280                 285

ACT GGA GAA AGT GGT CCA CGA GGA TTT CCA GGT CCA ATA GGT CCT CCG        972
Thr Gly Glu Ser Gly Pro Arg Gly Phe Pro Gly Pro Ile Gly Pro Pro
            290                 295                 300

GGT CTT AAA GGT GAT CGG GGA GCA ATT GGC TTT CCT GGA AGT CGA GGA       1020
Gly Leu Lys Gly Asp Arg Gly Ala Ile Gly Phe Pro Gly Ser Arg Gly
        305                 310                 315

CTC CCA GGA TAT GCC GGA AGG CCA GGA AAT TCT GGA CCA AAA GGC CAG       1068
Leu Pro Gly Tyr Ala Gly Arg Pro Gly Asn Ser Gly Pro Lys Gly Gln
    320                 325                 330

AAA GGG GAA AAG GGG AGT GGA AAC ACA TTA AGA CCA GTA CAA CTC ACT       1116
Lys Gly Glu Lys Gly Ser Gly Asn Thr Leu Arg Pro Val Gln Leu Thr
335                 340                 345                 350

GAT CAT ATT AGG GCA GGG CCC TCT TAA GATCAGGTGG GTTGGGCGGG             1163
Asp His Ile Arg Ala Gly Pro Ser  *
                355

ACATCCTCTG CTACCATCTC ATTAAAAGGC CCTTCACCTC TGGACAAGTC ATCTGCAACA     1223

ACTGACTTCC AAGATCCTTT TGTGACTCCT CCAAATGACT TTGGTTCCCG TGTTGTACCT     1283

GACTTCCACA TGGCCTTCTC TCCTGGTCCC TGGTGCTGTT TGGGCCTCTG CTCCCATGCT     1343

CATACCTCTT CTTACTCCAA TTAC                                            1367
```

Fig. 2B

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US96/08081

A. CLASSIFICATION OF SUBJECT MATTER

IPC(6) :Please See Extra Sheet.
US CL :Please See Extra Sheet.
According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 435/7.1, 7.21, 69.1, 240.1, 240.2, 240.23, 320.1; 530/300, 350; 536/23.1, 23.5

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

Please See Extra Sheet.

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	MATSUMOTO et al. Human macrophage scavenger receptors: Primary structure, expression, and localization in atherosclerotic lesions. Proc. Natl. Acad. Sci. December 1990, Vol. 87, pages 9133-9137, especially pages 9133-9136.	1-21
Y	SPRENGEL et al. Molecular Cloning and Expression of cDNA Encoding a Peripheral-type Benzodiazepine Receptor. Journal of Biological Chemistry. 05 December 1989, Vol. 264, No. 34 pages 20415-20421, especially page 20417.	1-21

[X] Further documents are listed in the continuation of Box C. [ ] See patent family annex.

* Special categories of cited documents:

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier document published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
16 AUGUST 1996	04 OCT 1996
Name and mailing address of the ISA/US Commissioner of Patents and Trademarks Box PCT Washington, D.C. 20231 Facsimile No. (703) 305-3230	Authorized officer KENNETH A. SORENSEN Telephone No. (703) 308-0196

Form PCT/ISA/210 (second sheet)(July 1992)*

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US96/08081

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	KODAMA et al. Type I macrophage scavenger receptor contains α-helical and collagen-like coiled coils. Nature. 08 February 1990, Vol. 343, pages 531-535, especially 531-534.	1-21

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US96/08081

A. CLASSIFICATION OF SUBJECT MATTER:
IPC (6):

G01N 33/53, 33/567; C12N 1/20, 5/00, 15/00; C07K 1/00, 21/04; A61K 38/00; C12P 21/06

A. CLASSIFICATION OF SUBJECT MATTER:
US CL :

435/7.1, 7.21, 69.1, 240.1, 240.2, 240.23, 320.1; 530/300, 350; 536/23.1, 23.5

B. FIELDS SEARCHED
Electronic data bases consulted (Name of data base and where practicable terms used):

CAPLUS, MEDLINE, BIOSIS, EMBASE, CONFSCI, DISSABS

search terms: 293 cells, cho cells, human macrophage scavenger receptor, human, msr